

FEATURES					
source	sinica,	128 Sec.	2 Yan-Chu-Yuan Road,	Taipei	11529, Taiwan
	location/Qualifiers				
gene	1..883				
sig_peptide	/organism="Rana catesbeiana"				
	/db_xref="taxon:8400"				
	/tissue_type="liver"				
CDS	1..883				
	/gene="rcr"				
	244..309				
	/gene="rcr"				
	244..645				
	/gene="rcr"				
	/note="stored in oocytes"				
	/codon_start=1				
	/product="ribonuclease precursor"				
	/protein_id="AAI0702.1"				
	/db_xref="GI:4204399"				
	/translation="MCASLLLVFGILGLSHLSLSONWATFQKHIIINPIINCNTT MDNNIYIVGGCKRVNFIIFISSATFYAICIGVINMNVLSITRPOLNCTPISITPRV CPYSRTETNYNICVKENQYPVHFAGICRCP" 310..642				
mat_peptide	/gene="rcr"				
	/function="pyrimidine-guanine sequence-specific RNase"				
	/function="cytotoxic agent against several tumor cells"				
	/product="ribonuclease"				
	/protein_id="AAI0702.1"				
	/db_xref="GI:4204399"				
polya_signal	827..832				
	/gene="rcr"				
BASE COUNT	285 a	186 c	150 g	262 t	
ORIGIN					
Query Match	57.9%	Score 191.2;	DB 5;	Length 883;	
Best Local Similarity	75.6%;	Pred. No. 1.2e-44;			
Matches 251; Conservative	0;	Mismatches 78;	Indels 3;	Gaps 1;	
Oy	1	cagaactggagcctacttcacgacgaagaacatcatcaccaaccgcgat--ctcgaac	57		
Db	310	CAGAActGGGCAACATTTCAGCAGAGCACATTAATAAACACCACCATCATCAACTGTAAAC	369		
Oy	58	actatcatggaacaacaacatctacatcgtltggtggtcagtgcgaacagtgtaaccttc	117		
Db	370	ACCATCATGGACAACAAATATATATATCGTAGAGGAGTGCAATGCAAGAGATGAACATTTC	429		
Oy	118	atcacctcttcgcgactactgctaaggctactcgtcactcgtggtatacaactgaagtt	177		
Db	430	ATAATTTCCTCTGCACAACACCGTGAAGGCCATCTGTACCGGGGTGATTAATVTGAATGA	489		
Oy	178	ctgtactactactcgttctcagctgaacacttcgaactcgtctactctatcacctccggtccg	237		
Db	490	TTAAGTACCCACAAAGATTCCAGCTCAAACTTCGACTCGATTCGATTCAACACCCGCCCT	549		
Oy	238	tgcgccgtactctcttcgtaactgaaaactactacatctcgtttaaatgcgaaaaccagtac	297		
Db	550	TGTCATCATTTAGCTCCAGAAACCGGAAAATTAATTAATGTAATGTAATGTAATTAAT	609		
Oy	298	ccggtcatttcgcgtgatacgtctgcgtccc	329		
Db	610	CCCCATCATTTTGTCTGGAATAGAGAGATGTCC	641		
RESULT	2				
AF351209		402 bp	DNA	linear	VRT 29-JUN-2001
LOCUS	Rana catesbeiana				
DEFINITION	Rana catesbeiana RNase A-type ribonuclease rc208 precursor, gene,				
ACCESSION	AF351209				
VERSION	AF351209.1				
KEYWORDS	bullfrog,				
SOURCE	Rana catesbeiana				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.				
REFERENCE	1 (bases 1 to 402)				

AUTHORS	Rosenberg, H. F., Zhang, J., Liao, Y. D. and Dyer, K. D.			
TITLE	Rapid diversification of RNase A superfamily ribonucleases from the bullfrog, <i>Rana catesbeiana</i>			
JOURNAL	J. Mol. Evol. 53 (1), 31-38 (2001)			
MEDLINE	21539506			
PUBMED	11683320			
REFERENCE	2 (bases 1 to 402)			
AUTHORS	Rosenberg, H. F., Zhang, J., Liao, Y. D. and Dyer, K. D.			
TITLE	Direct Submission			
JOURNAL	Submitted (21-FEB-2001) Laboratory of Host Defenses, NIAID, National Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20892, USA			
FEATURES	Location/Qualifiers			
source	1..402			
	/organism="Rana catesbeiana"			
	/db_xref="taxon:8400"			
sig_peptide	1..66			
mrna	<1..>402			
	/product="RNase A-type ribonuclease rc208 precursor"			
CDS	1..402			
	/codon_start=1			
	/product="RNase A-type ribonuclease rc208 precursor"			
	/protein_id="P4K30255.1"			
	/db_xref="GI:13560896"			
	/translation="MCASLLLVPGIILGLISHLSLSONMATEFOKHITNTSSINCVTI			
	MDNNYIVGGCKGVNTFIYISSATVVAITGVINMNVLSSTRPOLMTCRTITPRP			
	CPYSSRRYNNVICVCKENQYVHFAGIGRCP"			
BASE COUNT	120 a	93 c	75 g	114 t
ORIGIN				
Query Match	56.0%	Score 184.8;	DB 5;	Length 402;
Best Local Similarity	74.4%	Pred. No. 8.1e-43;		
Matches 247; Conservative	0;	Mismatches 82;	Indels 3;	Gaps 1;
Oy	1	cagaactggctactcttcagcagaacatcatcaactccg--atcatctgcac	57	
Db	67	CAGAACTGGCAACTTTCACGACAGACACTTACAAATACATCGAGCATCAACTGTAC	126	
Oy	58	actatcatgacaacaacatcatcatcgttggtygtcagtcagcaaacgtgttaacacttc	117	
Db	127	ACCATCATGACGAACAAATATATATCTGCGGAGAGTCAATCAAGGAGTGACACTTTC	186	
Oy	118	atcatctcttctgctactacactcgttaagcttatctgcactcgtgttataataacaaagtt	177	
Db	187	ATAATTCTTTGTGACACCAACCGTGAAGCCACTCTGTACCGGGGATGAATAATGAATGA	246	
Oy	178	ctgtctactactcgtttccagctgaacactgcacactcgttactctatcaactccgcgtccg	237	
Db	247	TTAAGTACACAAAGATTTCACACTCAACCTTGCACTGCTACTTCATTTACACCCCGGCT	306	
Oy	238	tgcgcgtactcttctcgttactggaactaactacatctgcgttgaatcgcgaaccagtgat	297	
Db	307	TGTCCATTTAGCTCCGAGAACGGAAATTAATTAACATATGTGTAAATGAGAAATCAATAT	366	
Oy	298	ccggttcatcttcgcgtgtatcgttcgttcgc	329	
Db	367	CCTGTACATTTTGGCTGGAAATAGACGATGTCC	398	
RESULT	3			
AF531210	402 bp DNA linear VRT 29-JUN-2001			
LOCUS	Rana catesbeiana RNase A-type ribonuclease rc212 precursor, gene,			
DEFINITION	complete cds.			
ACCESSION	AF531210			
VERSION	AF531210.1 GI:13560897			
KEYWORDS	bullfrog.			
SOURCE	Rana catesbeiana			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
REFERENCE	1 (bases 1 to 402)			
AUTHORS	Rosenberg, H. F., Zhang, J., Liao, Y. D. and Dyer, K. D.			

TITLE	Rapid diversification of RNase A superfamily ribonucleases from the bullfrog, <i>Rana catesbeiana</i>
JOURNAL	J. Mol. Evol. 53 (1), 51-58 (2001)
MEDLINE	21539506
PUBMED	11683320
REFERENCE	2 (bases 1 to 402)
AUTHORS	Rosenberg, H.F., Zhang, J., Liao, Y.-D. and Dyer, K.D.
JOURNAL	Submitted (21-FEB-2001) Laboratory of Host Defenses, NAID, National Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES	Location/Oualifiers
SOURCE	1..402
s1g_peptide	/organism="Rana catesbeiana"
mRNA	/db_xref="taxon:8400"
CDS	1..66 <1..>402 /product="RNase A-type ribonuclease rc212 precursor" 1..402 /codon_start=1 /product="RNase A-type ribonuclease rc212 precursor" /protein_id="AAK30256.1" /db_xref="GI:13560898" /translation="MCASPLLVGILVLSHSLSSNMATPFQOKHTITNSINCSNIMNNSLIVGGCKRVNFETASSLAVTSGYIDKVLSTFKQDLIRIFITPRP CPYSRETNVICYKCENQIPVRHAGIGCP"
BASE COUNT	120 a 94 c 76 g 112 t
ORIGIN	
Query Match	47.8% Score 157.6; DB 5; Length 402;
Best Local Similarity	69.3%; Pred. No. 5.9e-35;
Matches 230; Conservative	0; Mismatches 99; Indels 3; Gaps 1;
Oy	1 cagaactgggtactcttcacgaagaataatcatcaaccctcg---atcattgcac 57
Db	67 CAGAAGCTGGCAACATTTCAGCAGAGAACACTTAACAATFACATCGAGATCAACGTGAC 126
Oy	58 actaatgagacaacaacatctacatcgtytgtytgcagtgcaaacgyltaacatttc 117
Db	127 AACATCATGAACAACAGCTTATATTCGTGGGAGGTCAATGCAGAAAGTGAACTTTTC 186
Oy	118 atcatctctttgtctactactcgtttaagctatcttgcacctgtygtatatcaacatgaagt 177
Db	187 ATAGCTTCTTCTGCMAACCCGTGAAGGGCATCTGTACCGGGGTAAACGATAAAGAAATT 246
Oy	178 ctgtctactactcgtttccagctgaaacactgtgcactgtactctatcatactccggttcg 237
Db	247 TTAACTAGCACAAAATTCACAGCTGCACATTTTGACTCGTATTTTCATTACACC GCCCT 306
Oy	238 tgcgccgactctcttcgtactgaaactaactacactcgtgcgttaaatcgyaaaacagtag 297
Db	307 TGTCATCTTAGCTCCAGAAACGAAACTAATTAACATATGTGTAAAAATGTGAGAAATCAATAT 366
Oy	298 ccggtcatttcgctgctgatcggtcgttgcgc 329
Db	367 CCCGTACATTTTGTGGAATAGGACAAATGTCC 398
RESULT	4
LOCUS	AF351207 399 bp DNA linear VRT 29-JUN-2001
DEFINITION	Rana catesbeiana RNase A-type ribonuclease rc203 precursor, gene, complete cds.
ACCESSION	AF351207
VERSION	AF351207.1 GI:13560891
KEYWORDS	
SOURCE	bullfrog.
ORGANISM	Rana catesbeiana
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranae; Rana.
AUTHORS	Rosenberg, H.F., Zhang, J., Liao, Y.D. and Dyer, K.D.
TITLE	Rapid diversification of RNase A superfamily ribonucleases from the

FEATURES	source
JOURNAL	bullfrog, Rana catesbeiana
MEDLINE	J. Mol. Evol. 53 (1), 51-58 (2001)
PUBMED	21539506
REFERENCE	11683320
AUTHORS	2 (bases 1 to 399)
TITLE	Rosenberg, H.F., Zhang, J., Liao, Y.-D. and Dyer, K.D.
JOURNAL	Direct Submission
FEATURES	Submitted (21-FEB-2001) Laboratory of Host Defenses, NAID, National Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20892, USA
source	location/Qualifiers
	1..399
	/organism="Rana catesbeiana"
	/db_xref="taxon:8400"
sig_peptide	1..66
mRNA	<1..>399
CDS	/product="RNase A-type ribonuclease rc203 precursor"
	1..399
	/codon_start=1
	/product="RNase A-type ribonuclease rc203 precursor"
	/protein_id="RAK30253.1"
	/db_xref="GI:13560892"
	/translation="MCAKSLILVFGIILGLSHLSLSQTMARFOOKRIPSTSSINCNTI MDNNIVIVGGCKKVFNFIISSATFVAICNGVYNSVLSPTRRQDLTCTRTSTTPRP CPYSKRETKICKVCENQLPYHAGKGC"
BASE COUNT	123 a 94 c 73 g 109 t
ORIGIN	
Query Match	47.5% Score 156.6; DB 5; Length 399;
Best Local Similarity	70.0%; Pred. No. 1.2e-34;
Matches 226; Conservative	0; Mismatches 94; Indels 3; Gaps 1;
OY	1 cagaactgggactcttcacgcaagaacatcatcaacacccg---atcatctgcac 57
Db	67 CAGACCTGGGCAAAATTTCAGCAGAGACACATTCACACACATCGAGCATCACTGTAC 126
OY	58 actatcatgcaacaacatcatcatcgctggcgtagcagtgcaaacggttaacacttc 117
Db	127 ACCATCATGGACAAATATATATCTCGTGGAGGATCAATGCAAGATGACACTTTC 186
OY	118 atcatctcttcgtctactacactggttaagctctctgcactggtgtatataacatgaagtt 177
Db	187 ATAAATTCTTCTGCACACCGTGAAAGCCATCTGTAAAGGGGTGACAAATAGTAATGTA 246
OY	178 ctgtctactactcggttcacgtgaacactggaactgactctatctatctactccggtctg 237
Db	247 TTAACTGCCACAAGATTTCACAGCTGCACACTTGCACTCTACTTCCATTACACCCGCCCT 306
OY	238 tgcgccactctcttcgctactgaaactaactacatctgcgttaaatgcgaaacacgttac 297
Db	307 TGTCATATAGTATCCAAAGAAAGAAATTAAGATATGTGTAATAATGTGAGAAATCACTT 366
OY	298 ccggttcatcttcgctggtatcgg 320
Db	367 CCCGTACATTTTGTGTAATAGG 389
RESULT	5
LOCUS	AF351211
DEFINITION	AF351211 Rana catesbeiana RNase A-type ribonuclease rc203 precursor, gene, complete cds.
ACCESSION	AF351211
VERSION	AF351211.1
KEYWORDS	GI:13560899
ORGANISM	bullfrog.
SOURCE	Rana catesbeiana
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
REFERENCE	Rosenberg, H.F., Zhang, J., Liao, Y.D. and Dyer, K.D.
AUTHORS	1 (bases 1 to 402)
TITLE	Rapid diversification of Rana A superfamily ribonucleases from the

FEATURES	Source
JOURNAL	J. Mol. Evol. 53 (1), 31-38 (2001)
MEDLINE	21539506
REFERENCE	11683320
PUBMED	2 (bases 1 to 402)
AUTHORS	Rosenberg, H. F., Zhang, J., Liao, Y.-D. and Dyer, K. D.
TITLE	Direct Submission
JOURNAL	Submitted (21-FEB-2001) Laboratory of Host Defenses, NAID, National Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20892, USA
Source	Location/Qualifiers
	1..402
	/organism="Rana catesbeiana"
	/db_xref="taxon:8400"
slg_peptide	1..66
mRNA	<1..>402
CDS	/product="RNase A-typc ribonuclease rc218 precursor"
	1..402
	/codon_start=1
	/product="RNase A-typc ribonuclease rc218 precursor"
	/protein_id="AAK30257.1"
	/db_xref="GI:13560900"
	/translation="MCAKSLILVGGILGLSHLSLSONMATTFOEQHTTNSINCSNIMNLSLIVGGCKKVFNFVIASSATTVGATGSGVYDKVLSTKQDLICRIIFITPRP CPYSRPEITNVIKCEKNOYPVHRAGIGCP"
BASE COUNT	119 a 93 c 78 g 112 t
ORIGIN	

Query Match	46.8%	Score 154.4	DB 5	Length 402
Best Local Similarity	68.7%	Pred. No. 5e-34		
Matches 228	Conservative 0	Mismatches 101	Indels 3	Gaps 1
QY 1	cagaactggtgactcttcacgaagaaataatcatcaactccg---atcatctgcaac	57		
Db 67	CAGAACTGGGCACATTTCCAGAGACGACATTCGAATATCATGAGCATCAACGTGAC	126		
QY 58	actatcattggcacaacacatctacatcgctggctgctgcagtcgaacggttaacacttc	117		
Db 127	AACATCATGAACAACAGGTTATATATCGTGGAGGTCATCCAAAGAAAGTGACACTTTC	186		
QY 118	atcatcctcttcgtctactacgtttaagctatactgcactgtgttatataacatgaagtt	177		
Db 187	ATAGGCTTTCTGCAGACACCGTGAAAGGCATCTGTACCGGGGTACCGATTAAGAAATT	246		
QY 178	ctgtctactactcgcttcacgactgaacacttgcaactcgctactctatactccgctgcg	237		
Db 247	TTAAGTACACAAATTCACGACTCGACATTTGGACTCGTATTTTCATTACACCCCGCCT	306		
QY 238	tggccgctctctcttcgtcgtactgaactactacatctcgtttaatggaacacagctac	297		
Db 307	TGTCCATATTAACCTCCAGACGCGAAATCAATTACATATGTGTAAATGTGAAGATCAATAT	366		
QY 298	ccggtcattcgcgcgtgcgtatcgctcgttggcc	329		
Db 367	CCCCATATTTTGCCTGGAATAGGACAAATGCTCC	398		
RESULT 6	AF351208	399 bp	DNA	linear
LOCUS	Rana catesbeiana	RNase A-type	ribonuclease rc204	precursor, gene,
DEFINITION	complete cds.			
ACCESSION	AF351208			
VERSION	AF351208.1	GI:13560893		
KEYWORDS	.			
SOURCE	bullfrog.			
ORGANISM	Rana catesbeiana			
REFERENCE	Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.			
TITLE	(bases 1 to 399)			
JOURNAL	Rosenberg, H. F., Zhang, J., Liao, Y. D. and Dyer, K. D.			
	Rapid diversification of RNase A superfamily ribonucleases from the			
	bullfrog, Rana catesbeiana			
	J. Mol. Evol. 53 (1), 31-38 (2001)			

MEDLINE	21539506
PUBMED	11683320
REFERENCE	2 (bases 1 to 399)
AUTHORS	Rosenberg,H.E., Zhang,J., Liao,Y.-D. and Dyer,K.D.
TITLE	Direct Submission
JOURNAL	Submitted (21-FEB-2001) Laboratory of Host Defenses, NAID, National Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES	location/Qualifiers
SOURCE	1..399
	/organism="Rana catesbeiana"
	/db_xref="taxon:8400"
sig_peptide	1..66
mRNA	<1..>399
CDS	/product="RNase A-type ribonuclease rc204 precursor" 1..399 /codon_start=1 /product="RNase A-type ribonuclease rc204 precursor" /protein_id="AAK30254.1" /db_xref="GI:13560894" /translation="MCAKSLLVFGIILGLSHLSLSDQWPTFOOKHIPSTSIDCNTIMDDIYIVRCCKRVNTFIIFYSATVAICTGVLSNVSLSTRFQLXXRTFITSNP CPFSSTETNKICVCENEXEYPVHAGIGKC"
BASE COUNT	124 a 86 c 72 g 111 t 6 others
ORIGIN	

Query Match	45.2%;	Score 149;	DB 5;	Length 399;
Best Local Similarity	67.8%;	Pred. No. 1.8e-32;		
Matches 219;	Conservative 0;	Mismatches 101;	Indels 3;	Gaps 1;
Qy 1	cagaactgggactcttcacagcagaacaatcatcaaacctccgatac--ctgcac	57		
Dy 67	CAGAGCTGGCCAMACATTTTCACAGACACATTCACACATCATGAGCATGACTGTAC	126		
Qy 58	actatcatgagacaacaacatcatcatcgttggtgctcagtgcaacggtttaacacttc	117		
Dy 127	ACCATCATGGACAAAGACATATATATCTTAGAGGTCAATGCAGAAAGTCAACACTTTC	186		
Qy 118	atcatctctcttgctactactcgtgttaaagctatctgcactggtgttatcaacatgaagtt	177		
Dy 187	ATAATTATTTCTGCACACCCGTCAMGGCCATCTGTACCGGGGTGTMAATGTAATGTA	246		
Qy 178	ctgctactactcgttctcagctgaaacactgcactgcactgtactctatcatcccgctctc	237		
Dy 247	TTAAGTACCAACAATTCCTCCACTCAANNNNNCATCTGACTTTTCATTACATCCGCCCT	306		
Qy 238	tgcgcgtactctctcgtactgaaactactacatctcgtgttaaagtgcgaaaaccagtac	297		
Dy 307	TGTTCATTTACTGTCACAAAGAAAGTAATTAAGATATGTGTAATAATGGAATGAATAT	366		
Qy 298	ccggttcattctcgtggtatcgg	320		
Dy 367	CTGTACTTTTCTCTGGAATAGG	389		
RESULT 7				
AF288642				
LOCUS	AF288642	884 bp	DNA	linear VRT 08-AUG-2001
DEFINITION	Rana catesbeiana RC-RNaseII ribonuclease precursor, gene, complete cds.			
ACCESSION	AF288642			
VERSION	AF288642.2	GI:15111754		
KEYWORDS				
SOURCE				
ORGANISM				
	Rana catesbeiana			
	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
	1 (bases 1 to 884)			
	Liao, Y.D., Huang, H.C., Liu, Y.J., Wei, C.W., Tang, P.C. and Wang, S.C.			
	Purification and cloning of cytotoxic ribonucleases from Rana			
	catesbeiana (bullfrog)			
	JOURNAL			
	Nucleic Acids Res. 28 (21), 4097-4104 (2000)			
	MEDLINE			
	20512555			

REFERENCE	2 (bases 1 to 884)
AUTHORS	Liao Y.-D., Huang, H.-C., Leu, Y.-J., Wei, C.-W., Tang, P.-C. and Wang, S.-C.
TITLE	Direct Submission
JOURNAL	Submitted (18-JUL-2000) Institute of Biomedical Sciences, Academia Sinica, No.128 Sec.2 Yan-Chu-Yuan Road, Taipei 11529, Taiwan 3 (bases 1 to 884)
REFERENCE	Liao Y.-D., Huang, H.-C., Leu, Y.-J., Wei, C.-W., Tang, P.-C. and Wang, S.-C.
AUTHORS	Direct Submission
TITLE	Submitted (08-AUG-2001) Institute of Biomedical Sciences, Academia Sinica, No.128 Sec.2 Yan-Chu-Yuan Road, Taipei 11529, Taiwan
JOURNAL	Sequence update by submitter
REMARK	On Aug 8, 2001 this sequence version replaced gi:1118657.
COMMENT	
FEATURES	Location/Qualifiers
source	1..884
	/organism="Rana catesbeiana"
	/db_xref="taxon:8400"
	/tissue_type="liver"
mrna	1..685
	/product="RC-RNaseL1 ribonuclease precursor"
5'UTR	1..219
sig_peptide	220..282
CDS	220..618
	/codon_start=1
	/product="RC-RNaseL1 ribonuclease precursor"
	/protein_id="FAG30414.2"
	/db_xref="GI:15111755"
	/translation="MKASLLVFGFLGLSLSSONMAKFEKHITSTSSIDNTITDKAIYVIGKCKERNFTFIISSEGVKAIKCSVPDRKELSTSRKLNICIDSTIPRCEPHSPDNKKIKCKEKQLPVHVVGKIC"
	283..615
mat_peptide	/product="RC-RNaseL1 ribonuclease"
3'UTR	619..884
BASE COUNT	273 a 154 g 258 t
ORIGIN	
Query Match	36.2%; Score 119.6; DB 5; Length 884;
Best Local Similarity	64.7%; Pred. No. 6.1e-24;
Matches 211; Conservative 0; Mismatches 109; Indels 6; Gaps 2;	
QY 1	cagaactyggctactcttcacagcagaacaatatacatcaacactcgcatactc---tgcaac 57
DB 283	CAGAACTGGCGAAAATTTAAGAGAGACACATTACAGCACATCGACATCATTTGTAAC 342
QY 58	actatcatgagcaacaacatactacactgctgtgtgtgctagtgagaaacggttaacacttc 117
DB 343	ACTATCATGAGCAAAAGCCATATATATCGTAGAGGAAATGAAAGAACGGAAACCTTTC 402
QY 118	atcatctctcttgcctactacactggttaagctatctgcactgctgt---tatcaacatgaac 174
DB 403	ATCATTTCTTCTGAAAGACAGCTGAAGGCCATCTGTAGCGGGGTGTCAACCCGATAGGAAG 462
QY 175	gtctgttactactacgttttccagctggaacacttgcactgcacttactatcaactccoggt 234
DB 463	GAATTAAGTACACACAAAGTTTCAAACTCAACCTTCATTCGTGATTCATTCATTCACCCGCG 522
QY 235	ccggcgccgctactctcttcgcgtactggaactactatcatctcgtgttaaatgcaaacacag 294
DB 523	CGTGTCCATATACACCCAGCCCGGATATATATAAGATATGTGTAATAATGTGAGAAACA 582
QY 295	taccogctatcttcgcgtatcagc 320
DB 583	CTTCCCGTACATTTTGTGTGGAATAGG 608
RESULT 8	
LOCUS	AC005674 199450 bp DNA linear PRI 27-FEB-2001
DEFINITION	Human sapiens chromosome 4 clone RP11-448G15, complete sequence.
ACCESSION	AC005674
VERSION	AC005674.11 GI:13129492

KEYWORDS	HTG.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 199450)
JOURNAL	DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE	Direct Submission
AUTHORS	Unpublished
TITLE	2 (bases 1 to 199450)
JOURNAL	Stone,N.E., Schmitz,J.J., Cox,D.R. and Myers,R.M.
REFERENCE	Direct Submission
AUTHORS	Submitted (11-FEB-1998) Department of Genetics, Stanford Human
TITLE	Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA
JOURNAL	3 (bases 1 to 199450)
REFERENCE	DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS	Direct Submission
TITLE	Submitted (27-FEB-2001) DOE Joint Genome Institute, 2800 Mitchell
JOURNAL	Drive, Walnut Creek, CA 94598, USA
COMMENT	On Feb 27, 2001 this sequence version replaced gi:5757495.
	Finishing Completed at Stanford Human Genome Center
	www.shgc.stanford.edu
	Quality: Phrap Quality >=40 99.9% of Sequence;
	Estimated Total Number of Errors is 0.2.
	SFS Content:
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	SHGC-69010 G41975
	SHGC-50921 G33945
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	SHGC-1311 G33196.
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Matches 127; Conservative 0; Mismatches 136; Indels 0; Gaps 0;	
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RESULT 9	
H2067264	14235 bp DNA linear VRL 31-JAN-2001
LOCUS	H2067264
DEFINITION	Helicoverpa zea nuclear polyhedrosis virus, partial sequence.
ACCESSION	U67264.1
VERSION	U67264.1 GI:2078305
KEYWORDS	

SOURCE Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.
 ORGANISM Helicoverpa zea single nucleocapsid nucleopolyhedrovirus
 Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 Nucleopolyhedrovirus.
 REFERENCE 1 (bases 335 to 1075)
 AUTHORS Cowan, P., Bulach, D., Goodge, K., Robertson, A. and Tribe, D.E.
 TITLE Nucleotide sequence of the polyhedrin gene region of Helicoverpa zea single nucleocapsid nuclear polyhedrosis virus: placement of the virus in lepidopteran nuclear polyhedrosis virus group II
 JOURNAL J. Gen. Virol. 75 (Pt 11), 3211-3218 (1994)
 MEDLINE 95053907
 REFERENCE 2 (bases 1 to 14235)
 AUTHORS Le, T.H., Wu, T., Robertson, A., Bulach, D., Cowan, P., Goodge, K. and Tribe, D.
 TITLE Genetically variable triplet repeats in a RING-finger ORF of Helicoverpa species baculoviruses
 JOURNAL Virus Res. 49 (1), 67-77 (1997)
 MEDLINE 97321796
 PUBMED 9178498
 REFERENCE 3 (bases 1 to 14235)
 AUTHORS Le, T.H., Wu, T., Robertson, A., Bulach, D., Cowan, P., Goodge, K. and Tribe, D.
 TITLE Direct Submission
 JOURNAL Submitted (20-AUG-1996) Microbiology, U. of Melbourne, Grattan Street, Parkville, VIC 3052, Australia
 COMMENT On May 14, 1997 this sequence version replaced gi:60442 gi:454319.
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[illegible]

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
13	AC084361/c								
	172853 bp	DNA	linear	PRI 27-SEP-2001					
	12q BAC RP11-364C11	(Roswell Park Cancer Institute)							
	complete sequence.								
	AC084361								
	AC084361.19	GI:15027716							
	hg.								
	human.								
	homo sapiens								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
	1 (bases 1 to 172853)								
	Muzny D.M., Adams C., Adio-Ondola B., Alt-oman F.R., Allen C.,								
	Alsbrooks S.L., Amaraltinge H.C., Are J.R., Banks T., Barbara U.,								
	Benton J., Blmage K., Blankenburg K., Bonnah D., Bouck J.,								
	Bowie S., Brileva M., Brown E., Brown M., Bryant N.P., Bulay C.,								
	Burch P., Burkett C., Burrell K.L., Byrd N.C., Caron T.F.,								
	Carter M., Cavazos S.R., Chacko J., Chavez D., Chen G., Chen R.,								
	Chen Z., Chin D., Chowdhry I., Christopoulos C., Cleveland C.D.,								
	Cox C., Coyle M.D., Dathorne S.R., David R., Davila M.L., Davis C.,								
	Day-Carroll L., Dederich D.A., Delaney K.R., Delgado O.,								
	Dean A.L., Ding Y., Din H.H., Douthwaite K.J., Draper H.,								
	Dugan-Rocha S., Durbin K.J., Earhart C., Edgar D., Edwards C.C.,								
	Elhaj C., Emerling S., Escotto M., Falls T., Ferriguo D.,								
	Flagg N., Ford U., Foster P., Frantz P., Gabis A., Gao J.,								
	Garcia A., Garner T., Garza N., Gill R., Gorrall J.H., Guvera W.,								
	Gunaratne P., Hale S., Hamilton K., Han J., Harris C., Harris K.,								
	Hatt M., Havlik P., Hawes A., Hernandez J., Hernandez O.,								
	Hodgson A., Hogue M., Holloway C., Hollins B., Homsi F.,								
	Howard S., Huber J., Hulik S., Hume J., Ioshikhes I., Jackson L.E.,								
	Jacobson B., Jia Y., Johnson R., Jolivet S., Joudan S.,								
	Karlsson E., Kelly S., Khan U., King L., Korval T., Kovar C.,								
	Kratovic J., Kureshi A., Landry N., Leal B., Lee E., Lewis L.C.,								
	Lewis L., Li J., Li Z., Lichtarge O., Lieu C., Liu J., Liu W.,								
	Loulsaged H., Lozado R.J., Lu X., Lucier A., Lucier R., Luna R.,								
	Ma J., Maheshwari M., Mapua P., Marondel I., Martin R.,								
	Mattindale A., Martinez E., Massey E., Mawhney E., McLeod M.P.,								
	Meador M., Mei G., Mercher S., Metzger M., Miller A., Miner G.,								
	Miner Z., Mitchell T., Monabbat K., Montgomery K.T., Morgan M.,								
	Morris S., Moser M., Neal D., Nelson D., Newton J., Newton N.,								
	Nguyen A., Nguyen N., Nguyen N., Nickerson E., Nwokenwo S.,								
	Ough M., Okunou G., Oragunye N., Oyedro R., Pace A., Payton B.,								
	Peery J., Perez L., Peters L., Pickens R., Primus E., Pu L.L.,								
	Quiles M., Ren Y., Rives M., Rojs A., Rojndokhan I., Rolle M.,								
	Ruiz S., Savery G., Scherer S., Scott G., Shen H., Shm C.,								
	Shooshtari N., Sisson I., Sodergren E., Sonalike T., Sparks A.,								
	Stanley R., Stone H., Sutton A., Svatek A., Taboor P., Tamerisa A.,								
	Tamerisa K., Thoms S., Usmani K., Vasquez L., Vera V., Villalona D.,								
	Vinson R., Wall R., Wang S., Ward-Moore S., Warren R.,								
	Washington C., Wallington S., Williams G., Williamson A.,								
	Waczzyk R., Wooden S., Worley K., Wu C., Wu Y., Wu Y.F., Zhou J.,								
	Zorilla S., Kuchierapatti R., Weinstein G. and Gibbs R.								

COMMENT

Baylor Plaza, Houston, TX 77030, USA
 On Jul 28, 2001 this sequence version replaced g1:14861680.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc_help@bcm.tmc.edu
 CLONE LENGTH: This sequence does not necessarily represent the
 entire insert of this clone. Overlapping regions of clones are only
 sequenced and submitted once, so the sequence for the remainder of
 the insert may be found in the record for the adjacent clones.
 Overlapping clones are noted at the beginning and end of the
 features listing.

ANNOTATION OF FEATURES:

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished) for Human and Mouse sequences. <http://www.repeatmasker.org/> The sites of repeats are identified using ePCR (genome Res. 11:541-550) searches of a local database that includes entries from DDB, GDB, and local mapping efforts.

GENES AND CDNA SEQUENCES. Genes demonstrated at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE. Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

11

SOURCE	Location/Qualifiers
	1. .172853

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repeat_region	complement(2. .154)
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/rpt_family="MIR"

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repeat_region 1663.1832
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repeat_region
complete(13/2: :2
/rpt family="MIR"
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repeat region
  complement(2971
    /1pc_1ability=L2
  )
  3
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repeat_region 34/4. .3525
/rot fam11ws"MTB"
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/rpt_family="MLT1I

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repeat_region 5059.  .5355
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/rpt_family="MIR"

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repeat_region      5578..5598
                    /rpt_family="AT_rich"
repeat_region      complement(5697..5795)
                    /rpt_family="L2"
repeat_region      complement(6215..6472)
                    /rpt_family="MIR"
repeat_region      7183..7560
                    /rpt_family="MER69"
repeat_region      complement(8700..8878)
                    /rpt_family="MER5B"
repeat_region      8917..9111
                    /rpt_family="MIR"
repeat_region      9212..9324
                    /rpt_family="MIR"
repeat_region      10745..10794
                    /rpt_family="CT-rich"
repeat_region      complement(10981..11063)
                    /rpt_family="MIR"
repeat_region      11214..11412
                    /rpt_family="MIR"
repeat_region      11474..11741
                    /rpt_family="AluYo"
repeat_region      12403..12453
                    /rpt_family="(CA)n"
repeat_region      12879..13046
                    /rpt_family="MIR"
repeat_region      complement(13049..13119)
                    /rpt_family="L2"
repeat_region      13376..13412
                    /rpt_family="L2"
repeat_region      complement(13414..13706)
                    /rpt_family="Alu5x"
repeat_region      13854..14213
                    /rpt_family="L1ME"
repeat_region      complement(14639..14859)
                    /rpt_family="MER20"
repeat_region      14978..14999
                    /rpt_family="AT_rich"
repeat_region      15220..15387
                    /rpt_family="MIR"
repeat_region      complement(16602..16719)
                    /rpt_family="MIR"
repeat_region      complement(17029..17225)
                    /rpt_family="L1ME"
repeat_region      complement(17402..17591)
                    /rpt_family="L1ME"
repeat_region      18302..18502
                    /rpt_family="L1ME3A"
repeat_region      18542..18863
                    /rpt_family="L2"
repeat_region      complement(18973..19096)
                    /rpt_family="L1P1"
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repeat_region      19300..19687
                    /rpt_family="MLT1C"

Query Match      13.1% Score 43.2; DB 9; Length 172853;
Best Local Similarity 56.2% Pred. No. 0.12; Mismatches 63; Indels 0; Gaps 0;
Matches 81; Conservative 0;

```

RESULT 14 AC073376/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AC073376 178150 bp DNA linear HTG 28-JUN-2000
Homo sapiens clone RP11-173C19, WORKING DRAFT SEQUENCE, 37
unordered pieces.
AC073376 2 GI:8780662
AC073376 HTG: HTGS_PHASE1; HTGS_DRAFT.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 178150)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-173C19
Unpublished
2 (bases 1 to 178150)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Bouckgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., Dearlano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domingo,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Laroque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., MacDonald,P., Margis,N.,
McCarthy,M., McKean,P., McGuire,A., McKernan,K., McPheters,R.,
Meldrum,J., Meneus,L., Minova,T., Miranda,C., Mleaga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Sudramanian,A., Talamas,J.,
Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trifillo,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (15-JUN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 28, 2000 this sequence version replaced gi:8567832.
All repeats were identified using RepeatMasker:
smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE JOURNAL COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L10415
Center clone name: 173_C_19
----- Summary Statistics -----
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 158085 bases at least Q40
Consensus quality: 168416 bases at least Q30
Consensus quality: 172386 bases at least Q20
Insert size: 174550; sum-of-contigs
Quality coverage: 3.5 in Q20 bases; sum-of-contigs
----- NOTE: This is a 'working draft' sequence. It currently
* consists of 37 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1157: contig of 1157 bp in length

[illegible]

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source
1. .178150
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/db_xref="taxon:9606"
/clone="RP11-173C19"
/clone_lib="RPCr-11 Human Male BAC"

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1258. .2373
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3883. .5365
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13671. .15247
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19912. .21770
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misc_feature
21871. .23629
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vector_slide:right"

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23730. .25971
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misc_feature
26072. .28405
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32532. .36946
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37047. .41156
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56793. .60975
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Query Match      13.1%; Score 43.2; DB 2; Length 178150;
Best Local Similarity 56.2%; Pred. No. 0.12;
Matches 81; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
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RESULT 15
AC099636/c
LOCUS 155765 bp DNA linear HTG 16-NOV-2001
DEFINITION Mus musculus clone RP24-149H13, WORKING DRAFT SEQUENCE, 20
 unordered pieces.
ACCESSION AC099636
VERSION AC099636.1 GI:16948003
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 155765)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Unpublished
JOURNAL 2 (bases 1 to 155765)
REFERENCE 2 (bases 1 to 155765)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,
 Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
 Choquel, Y., Collangelo, M., Collins, S., Collymore, A., Cook, A.,
 Cooke, P., Dearrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
 Ferreira, P., Fitzhugh, N., Gage, D., Galagan, J., Gaidyna, S.,
 Glinde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
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 Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
 Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
 McCarthy, M., McKean, P., McKernan, K., McPheters, R., Meldrum, J.,
 Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
 Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
 Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, D.,
 Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
 Roman, J., Roselli, M., Roy, A., Santos, R., Schauer, S., Schpack, R.,
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, K., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliou, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.D., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
COMMENT Direct Submission
 Submitted (16-NOV-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
TITLE Genome Center
JOURNAL Center: Whitehead Institute/ MIT Center for Genome Research
COMMENT Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
Project Information
 Center project name: L17403
 Center clone name: 149_H13
Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 149108 bases at least Q40
 Consensus quality: 152022 bases at least Q20
 Consensus quality: 153025 bases at least Q20
 Insert size: 158000; agarose-fp
 Insert size: 153865; sum-of-contigs
 Quality coverage: 12.8 in Q20 bases; sum-of-contigs
 Quality coverage: 13.1 in Q20 bases; sum-of-contigs
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 20 contigs. The true order of the pieces
 * is not known and their order in this sequence reflects
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence

* as soon as it is available and the accession number will
 * be preserved.
 1 8420: contig of 8420 bp in length
 * 8421 8520: gap of 100 bp
 * 8521 9147: contig of 627 bp in length
 * 9148 9247: gap of 100 bp
 * 9248 9881: contig of 634 bp in length
 * 9882 9981: gap of 100 bp
 * 9982 10632: contig of 651 bp in length
 * 10633 10732: gap of 100 bp
 * 10733 11428: contig of 696 bp in length
 * 11429 11528: gap of 100 bp
 * 11529 12139: contig of 611 bp in length
 * 12140 12239: gap of 100 bp
 * 12240 12867: contig of 628 bp in length
 * 12868 12967: gap of 100 bp
 * 12968 14377: contig of 1410 bp in length
 * 14378 14477: gap of 100 bp
 * 14478 15555: contig of 1078 bp in length
 * 15556 15655: gap of 100 bp
 * 15656 16770: contig of 1115 bp in length
 * 16771 16870: gap of 100 bp
 * 16871 17550: contig of 680 bp in length
 * 17551 17650: gap of 100 bp
 * 17651 20264: contig of 2614 bp in length
 * 20265 20364: gap of 100 bp
 * 20365 22093: contig of 1729 bp in length
 * 22094 22193: gap of 100 bp
 * 22194 23381: contig of 1188 bp in length
 * 23382 23481: gap of 100 bp
 * 23482 72883: contig of 49402 bp in length
 * 72884 72983: gap of 100 bp
 * 72984 85260: contig of 12277 bp in length
 * 85261 85360: gap of 100 bp
 * 85361 103628: contig of 18268 bp in length
 * 103629 103728: gap of 100 bp
 * 103729 124191: contig of 20463 bp in length
 * 124192 124291: gap of 100 bp
 * 124292 148926: contig of 24635 bp in length
 * 148927 149026: gap of 100 bp
 * 149027 155765: contig of 6739 bp in length.
FEATURES
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